

SEQUENCE LISTING



<110> Feder, John N.
Mintier, Gabe
Kinney, Gene G
Ramanathan, Chandra S

<120> NOVEL IMIDAZOLINE RECEPTOR HOMOLOGS

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<141> 2001-08-17

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Trp	Arg	Pro	Leu	Phe	Gln	Lys	Thr	Glu	Ser	Pro	Ala	Val	Cys	Pro	Asn	
705					710					715					720	

Cys	Gly	Ser	Asp	His	Val	Val	Leu	Leu	Ala	Val	Ser	Arg	Gly	Thr	Pro	
				725					730					735		
Asn	Arg	Glu	Arg	Lys	Gln	Gly	Glu	Gln	Ser	Leu	Ala	Pro	Ser	Pro	Phe	
				740				745					750			
Ala	Ser	Pro	Val	Cys	His	Pro	Pro	Gly	His	Gly	Asp	His	Leu	Asp	Arg	
		755					760					765				
Ala	Lys	Asn	Ser	Pro	Pro	Gln	Ala	Pro	Ser	Thr	Arg	Asp	His	Gly	Ser	
		770				775					780					
Trp	Ser	Leu	Ser	Pro	Pro	Pro	Glu	Arg	Cys	Gly	Leu	Arg	Ser	Val	Asp	
785				790						795					800	
His	Arg	Leu	Arg	Leu	Phe	Leu	Asp	Val	Glu	Val	Phe	Ser	Asp	Ala	Gln	
				805					810					815		
Glu	Glu	Phe	Gln	Cys	Cys	Leu	Lys	Val	Pro	Val	Ala	Leu	Ala	Gly	His	
			820					825					830			

Thr Gly Glu Phe Met Cys Leu Val Val Val Ser Asp Arg Arg Leu Tyr
835 840 845

Leu Leu Lys Val Thr Gly Glu Met Arg Glu Pro Pro Ala Ser Trp Leu
850 855 860

Gln Leu Thr Leu Ala Val Pro Leu Gln Asp Leu Ser Gly Ile Glu Leu
865 870 875 880

Gly Leu Ala Gly Gln Ser Leu Arg Leu Glu Trp Ala Ala Gly Ala Gly
885 890 895

Arg Cys Val Leu Leu Pro Arg Asp Ala Arg His Cys Arg Ala Phe Leu
900 905 910

Glu Glu Leu Leu Asp Val Leu Gln Ser Leu Pro Pro Ala Trp Arg Asn
915 920 925

Cys Val Ser Ala Thr Glu Glu Glu Val Thr Pro Gln His Arg Leu Trp
930 935 940

Pro Leu Leu Glu Lys Asp Ser Ser Leu Glu Ala Arg Gln Phe Phe Tyr
945 950 955 960

Leu Arg Ala Phe Leu Val Glu Gly Pro Ser Thr Cys Leu Val Ser Leu
965 970 975

Leu Leu Thr Pro Ser Thr Leu Phe Leu Leu Asp Glu Asp Ala Ala Gly
980 985 990

Ser Pro Ala Glu Pro Ser Pro Pro Ala Ala Ser Gly Glu Ala Ser Glu
995 1000 1005

Lys Val Pro Pro Ser Gly Pro Gly Pro Ala Val Arg Val Arg Glu Gln
1010 1015 1020

Gln Pro Leu Ser Ser Leu Ser Ser Val Leu Leu Tyr Arg Ser Ala Pro
1025 1030 1035 1040

Glu Asp Leu Arg Leu Leu Phe Tyr Asp Glu Val Ser Arg Leu Glu Ser
1045 1050 1055

Phe Trp Ala Leu Arg Val Val Cys Gln Glu Gln Leu Thr Ala Leu Leu
1060 1065 1070

Ala Trp Ile Arg Glu Pro Trp Glu Glu Leu Phe Ser Ile Gly Leu Arg
1075 1080 1085

Thr Val Ile Gln Glu Ala Leu Ala Leu Asp Arg
1090 1095

<210> 5

<211> 20

<212> DNA

<213> Homo sapiens

<400> 5
gctggagacc ctgatttgca

20

<210> 6
<211> 23
<212> DNA
<213> Homo sapiens

<400> 6
tggacttgat tgtggcttag gtt

23

<210> 7
<211> 1504
<212> PRT
<213> Homo sapiens

<220>
<223> DATABASE ACCESSION NUMBER: Database: Genbank,
accession number: NP_009115

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Lys Glu Ala Arg Val Val Gly Ser Glu Leu Val Asp Thr Tyr Thr Val
20 25 30
Tyr Ile Ile Gln Val Thr Asp Gly Ser His Glu Trp Thr Val Lys His
35 40 45
Arg Tyr Ser Asp Phe His Asp Leu His Glu Lys Leu Val Ala Glu Arg
50 55 60
~~Lys Ile Asp Lys Asn Leu Leu Pro Pro Lys Lys Ile Ile Gly Lys Asn~~
65 70 75 80
Ser Arg Ser Leu Val Glu Lys Arg Glu Lys Asp Leu Glu Val Tyr Leu
85 90 95
Gln Lys Leu Leu Ala Ala Phe Pro Gly Val Thr Pro Arg Val Leu Ala
100 105 110
His Phe Leu His Phe His Phe Tyr Glu Ile Asn Gly Ile Thr Ala Ala
115 120 125
Leu Ala Glu Glu Leu Phe Glu Lys Gly Glu Gln Leu Leu Gly Ala Gly
130 135 140
Glu Val Phe Ala Ile Gly Pro Leu Gln Leu Tyr Ala Val Thr Glu Gln
145 150 155 160
Leu Gln Gln Gly Lys Pro Thr Cys Ala Ser Gly Asp Ala Lys Thr Asp
165 170 175
Leu Gly His Ile Leu Asp Phe Thr Cys Arg Leu Lys Tyr Leu Lys Val

180					185					190						
Ser	Gly	Thr	Glu	Gly	Pro	Phe	Gly	Thr	Ser	Asn	Ile	Gln	Glu	Gln	Leu	
195					200					205						
Leu	Pro	Phe	Asp	Leu	Ser	Ile	Phe	Lys	Ser	Leu	His	Gln	Val	Glu	Ile	
210					215					220						
Ser	His	Cys	Asp	Ala	Lys	His	Ile	Arg	Gly	Leu	Val	Ala	Ser	Lys	Pro	
225					230					235					240	
Thr	Leu	Ala	Thr	Leu	Ser	Val	Arg	Phe	Ser	Ala	Thr	Ser	Met	Lys	Glu	
245					250					255						
Val	Leu	Val	Pro	Glu	Ala	Ser	Glu	Phe	Asp	Glu	Trp	Glu	Pro	Glu	Gly	
260					265					270						
Thr	Thr	Leu	Glu	Gly	Pro	Val	Thr	Ala	Val	Ile	Pro	Thr	Trp	Gln	Ala	
275					280					285						
Leu	Thr	Thr	Leu	Asp	Leu	Ser	His	Asn	Ser	Ile	Ser	Glu	Ile	Asp	Glu	
290					295					300						
Ser	Val	Lys	Leu	Ile	Pro	Lys	Ile	Glu	Phe	Leu	Asp	Leu	Ser	His	Asn	
305					310					315					320	
Gly	Leu	Leu	Val	Val	Asp	Asn	Leu	Gln	His	Leu	Tyr	Asn	Leu	Val	His	
325					330					335						
Leu	Asp	Leu	Ser	Tyr	Asn	Lys	Leu	Ser	Ser	Leu	Glu	Gly	Leu	His	Thr	
340					345					350						
Lys	Leu	Gly	Asn	Ile	Lys	Thr	Leu	Asn	Leu	Ala	Gly	Asn	Leu	Leu	Glu	
355					360					365						
Ser Leu Ser Gly Leu His Lys Leu Tyr Ser Leu Val Asn Leu Asp Leu																
370					375					380						
Arg	Asp	Asn	Arg	Ile	Glu	Gln	Met	Glu	Glu	Val	Arg	Ser	Ile	Gly	Ser	
385					390					395					400	
Leu	Pro	Cys	Leu	Glu	His	Val	Ser	Leu	Leu	Asn	Asn	Pro	Leu	Ser	Ile	
405					410					415						
Ile	Pro	Asp	Tyr	Arg	Thr	Lys	Val	Leu	Ala	Gln	Phe	Gly	Glu	Arg	Ala	
420					425					430						
Ser	Glu	Val	Cys	Leu	Asp	Asp	Thr	Val	Thr	Thr	Glu	Lys	Glu	Leu	Asp	
435					440					445						
Thr	Val	Glu	Val	Leu	Lys	Ala	Ile	Gln	Lys	Ala	Lys	Glu	Val	Lys	Ser	
450					455					460						
Lys	Leu	Ser	Asn	Pro	Glu	Lys	Lys	Gly	Gly	Glu	Asp	Ser	Arg	Leu	Ser	
465					470					475					480	
Ala	Ala	Pro	Cys	Ile	Arg	Pro	Ser	Ser	Ser	Pro	Pro	Thr	Val	Ala	Pro	

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cont

485										490					495				
Ala	Ser	Ala	Ser	Leu	Pro	Gln	Pro	Ile	Leu	Ser	Asn	Gln	Gly	Ile	Met				
			500						505					510					
Phe	Val	Gln	Glu	Glu	Ala	Leu	Ala	Ser	Ser	Leu	Ser	Ser	Thr	Asp	Ser				
		515					520						525						
Leu	Thr	Pro	Glu	His	Gln	Pro	Ile	Ala	Gln	Gly	Cys	Ser	Asp	Ser	Leu				
	530					535					540								
Glu	Ser	Ile	Pro	Ala	Gly	Gln	Ala	Ala	Ser	Asp	Asp	Leu	Arg	Asp	Val				
545					550					555					560				
Pro	Gly	Ala	Val	Gly	Gly	Ala	Ser	Pro	Glu	His	Ala	Glu	Pro	Glu	Val				
				565					570					575					
Gln	Val	Val	Pro	Gly	Ser	Gly	Gln	Ile	Ile	Phe	Leu	Pro	Phe	Thr	Cys				
			580					585						590					
Ile	Gly	Tyr	Thr	Ala	Thr	Asn	Gln	Asp	Phe	Ile	Gln	Arg	Leu	Ser	Thr				
		595					600						605						
Leu	Ile	Arg	Gln	Ala	Ile	Glu	Arg	Gln	Leu	Pro	Ala	Trp	Ile	Glu	Ala				
	610					615					620								
Ala	Asn	Gln	Arg	Glu	Glu	Gly	Gln	Gly	Glu	Gln	Gly	Glu	Glu	Glu	Asp				
625					630					635					640				
Glu	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Val	Ala	Glu	Asn	Arg	Tyr	Phe	Glu				
				645					650					655					
Met	Gly	Pro	Pro	Asp	Val	Glu	Glu	Glu	Glu	Gly	Gly	Gly	Gln	Gly	Glu				
			660					665					670						
Glu	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Glu	Glu	Ala	Glu	Glu	Glu	Arg	Leu				
			675					680						685					
Ala	Leu	Glu	Trp	Ala	Leu	Gly	Ala	Asp	Glu	Asp	Phe	Leu	Leu	Glu	His				
			690			695					700								
Ile	Arg	Ile	Leu	Lys	Val	Leu	Trp	Cys	Phe	Leu	Ile	His	Val	Gln	Gly				
705				710							715				720				
Ser	Ile	Arg	Gln	Phe	Ala	Ala	Cys	Leu	Val	Leu	Thr	Asp	Phe	Gly	Ile				
				725					730					735					
Ala	Val	Phe	Glu	Ile	Pro	His	Gln	Glu	Ser	Arg	Gly	Ser	Ser	Gln	His				
			740					745						750					
Ile	Leu	Ser	Ser	Leu	Arg	Phe	Val	Phe	Cys	Phe	Pro	His	Gly	Asp	Leu				
	755						760						765						
Thr	Glu	Phe	Gly	Phe	Leu	Met	Pro	Glu	Leu	Cys	Leu	Val	Leu	Lys	Val				
	770					775					780								
Arg	His	Ser	Glu	Asn	Thr	Leu	Phe	Ile	Ile	Ser	Asp	Ala	Ala	Asn	Leu				

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Cont

785	790	795	800
His Glu Phe His	Ala Asp Leu Arg Ser Cys Phe Ala Pro Gln His Met		
	805	810	815
Ala Met Leu Cys Ser Pro Ile Leu Tyr Gly Ser His Thr Ser Leu Gln			
	820	825	830
Glu Phe Leu Arg Gln Leu Leu Thr Phe Tyr Lys Val Ala Gly Gly Cys			
	835	840	845
Gln Glu Arg Ser Gln Gly Cys Phe Pro Val Tyr Leu Val Tyr Ser Asp			
	850	855	860
Lys Arg Met Val Gln Thr Ala Ala Gly Asp Tyr Ser Gly Asn Ile Glu			
	865	870	875
Trp Ala Ser Cys Thr Leu Cys Ser Ala Val Arg Arg Ser Cys Cys Ala			
	885	890	895
Pro Ser Glu Ala Val Lys Ser Ala Ala Ile Pro Tyr Trp Leu Leu Leu			
	900	905	910
Thr Pro Gln His Leu Asn Val Ile Lys Ala Asp Phe Asn Pro Met Pro			
	915	920	925
Asn Arg Gly Thr His Asn Cys Arg Asn Arg Asn Ser Phe Lys Leu Ser			
	930	935	940
Arg Val Pro Leu Ser Thr Val Leu Leu Asp Pro Thr Arg Ser Cys Thr			
	945	950	955
Gln Pro Arg Gly Ala Phe Ala Asp Gly His Val Leu Glu Leu Leu Val			
	965	970	975
Gly Tyr Arg Phe Val Thr Ala Ile Phe Val Leu Pro His Glu Lys Phe			
	980	985	990
His Phe Leu Arg Val Tyr Asn Gln Leu Arg Ala Ser Leu Gln Asp Leu			
	995	1000	1005
Lys Thr Val Val Ile Ala Lys Thr Pro Gly Thr Gly Gly Ser Pro Gln			
	1010	1015	1020
Gly Ser Phe Ala Asp Gly Gln Pro Ala Glu Arg Arg Ala Ser Asn Asp			
	1025	1030	1035
Gln Arg Pro Gln Glu Val Pro Ala Glu Ala Leu Ala Pro Ala Pro Val			
	1045	1050	1055
Glu Val Pro Ala Pro Ala Pro Ala Ala Ala Ser Ala Ser Gly Pro Ala			
	1060	1065	1070
Lys Thr Pro Ala Pro Ala Glu Ala Ser Thr Ser Ala Leu Val Pro Glu			
	1075	1080	1085
Glu Thr Pro Val Glu Ala Pro Ala Pro Pro Pro Ala Glu Ala Pro Ala			

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1090	1095	1100
Gln Tyr Pro Ser Glu His Leu Ile Gln Ala Thr Ser Glu Glu Asn Gln 1105 1110 1115 1120		
Ile Pro Ser His Leu Pro Ala Cys Pro Ser Leu Arg His Val Ala Ser 1125 1130 1135		
Leu Arg Gly Ser Ala Ile Ile Glu Leu Phe His Ser Ser Ile Ala Glu 1140 1145 1150		
Val Glu Asn Glu Glu Leu Arg His Leu Met Trp Ser Ser Val Val Phe 1155 1160 1165		
Tyr Gln Thr Pro Gly Leu Glu Val Thr Ala Cys Val Leu Leu Ser Thr 1170 1175 1180		
Lys Ala Val Tyr Phe Val Leu His Asp Gly Leu Arg Arg Tyr Phe Ser 1185 1190 1195 1200		
Glu Pro Leu Gln Asp Phe Trp His Gln Lys Asn Thr Asp Tyr Asn Asn 1205 1210 1215		
Ser Pro Phe His Ile Ser Gln Cys Phe Val Leu Lys Leu Ser Asp Leu 1220 1225 1230		
Gln Ser Val Asn Val Gly Leu Phe Asp Gln His Phe Arg Leu Thr Gly 1235 1240 1245		
Ser Thr Pro Met Gln Val Val Thr Cys Leu Thr Arg Asp Ser Tyr Leu 1250 1255 1260		
Thr His Cys Phe Leu Gln His Leu Met Val Val Leu Ser Ser Leu Glu 1265 1270 1275 1280		
Arg Thr Pro Ser Pro Glu Pro Val Asp Lys Asp Phe Tyr Ser Glu Phe 1285 1290 1295		
Gly Asn Lys Thr Thr Gly Lys Met Glu Asn Tyr Glu Leu Ile His Ser 1300 1305 1310		
Ser Arg Val Lys Phe Thr Tyr Pro Ser Glu Glu Glu Ile Gly Asp Leu 1315 1320 1325		
Thr Phe Thr Val Ala Gln Lys Met Ala Glu Pro Glu Lys Ala Pro Ala 1330 1335 1340		
Leu Ser Ile Leu Leu Tyr Val Gln Ala Phe Gln Val Gly Met Pro Pro 1345 1350 1355 1360		
Pro Gly Cys Cys Arg Gly Pro Leu Arg Pro Lys Thr Leu Leu Leu Thr 1365 1370 1375		
Ser Ser Glu Ile Phe Leu Leu Asp Glu Asp Cys Val His Tyr Pro Leu 1380 1385 1390		
Pro Glu Phe Ala Lys Glu Pro Pro Gln Arg Asp Arg Tyr Arg Leu Asp		

1395

1400

1405

Asp Gly Arg Arg Val Arg Asp Leu Asp Arg Val Leu Met Gly Tyr Gln
 1410 1415 1420

Thr Tyr Pro Gln Ala Leu Thr Leu Val Phe Asp Asp Val Gln Gly His
 1425 1430 1435 1440

Asp Leu Met Gly Ser Val Thr Leu Asp His Phe Gly Glu Val Pro Gly
 1445 1450 1455

Gly Pro Ala Arg Ala Ser Gln Gly Arg Glu Val Gln Trp Gln Val Phe
 1460 1465 1470

Val Pro Ser Ala Glu Ser Arg Glu Lys Leu Ile Ser Leu Leu Ala Arg
 1475 1480 1485

Gln Trp Glu Ala Leu Cys Gly Arg Glu Leu Pro Val Glu Leu Thr Gly
 1490 1495 1500

<210> 8

<211> 100

<212> DNA

<213> Homo sapiens

<220>

<223> OTHER INFORMATION: The nucleotide sequence is
 nucleotides 1644 to 1743 of Incyte clone 2499870
 DATABASE ACCESSION NUMBER: Database: Incyte,
 Accession number: 2499870

<400> 8

tacgctgtgg ccattgagttc aagccagagg agcccaggat gggattagac agtgaggaag 60
 gctggaggcc tctgttccaa aagacagaat ctctgtctgt 100

<210> 9

<211> 100

<212> DNA

<213> Homo sapiens

<220>

<223> Other Information: The nucleotide sequence is
 nucleotides 1794 to 1893 of Incyte clone 2499870
 DATABASE ACCESSION NUMBER: Database: Incyte,
 Accession number: 2499870

<400> 9

gaacccccaa cagggagcgg aaacagggag agcagtcctt ggctccttct ccgtttgccca 60
 gccctgtctg ccaccctcct ggccatggtg accaccttga 100

<210> 10

<211> 103
<212> DNA
<213> Homo sapiens

<220>
<223> OTHER INFORMATION: The nucleotide sequence is
nucleotides 2444 to 2546 of Incyte clone 2499870
DATABASE ACCESSION NUMBER: Database: Incyte,
Accession number: 2499870

<400> 10
tcataccttgaggctcgcca gttcttctac cttcgggcgt tcctggttga aggcccttcc 60
acctgcctcg tatccctgtt gctgactccg tccacctgt tcc 103

<210> 11
<211> 1289
<212> PRT
<213> Drosophila melanogaster

<220>
<223> DATABASE ACCESSION NUMBER: Database: Genbank,
Accession: AAF52305

<400> 11
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Gly Asp Lys Ile Leu Ser Ser Glu Phe Thr Leu Thr Leu Ser Gly Ser
20 25 30
Leu Leu Arg Ala Leu Asn Asp Ser Phe Thr Leu Ile Ala Asp Thr Glu
35 40 45
Ile Gly Thr Gly Ala Gly Tyr Leu Gln Pro Gln Ser Phe Gln Val Val
50 55 60

Lys Pro Ile Asn Ala Lys Ser Ser Val Phe Pro Asp Leu Gln Leu Val
65 70 75 80

His Asp Phe Val Gln Lys Thr Thr Leu Leu Lys Leu Thr Tyr Phe Pro
85 90 95

Ser Glu His Tyr Phe Glu Gly Ala Ile Asp Ile Ala Lys Phe Arg Ala
100 105 110

Leu Arg Arg Leu Glu Val Asn Lys Ile Asn Ile Gly Gln Val Val Gly
115 120 125

Ile Gln Pro Leu Arg Gly Gln Leu Gln His Leu Ile Cys Val Lys Ser
130 135 140

Leu Thr Ser Val Asp Asp Ile Ile Thr Arg Cys Gly Gly Asp Asn Ser
145 150 155 160

Asn Gly Phe Val Trp Asn Glu Leu Lys Thr Ala Asp Phe Ser Tyr Asn
165 170 175

Ser Leu Arg Ser Val Asp Thr Ala Leu Glu Phe Ala Gln His Leu Gln
180 185 190

His Leu Asn Leu Arg His Asn Lys Leu Thr Ser Val Ala Ala Ile Lys
195 200 205

Trp Leu Pro His Leu Lys Thr Leu Asp Leu Ser Tyr Asn Cys Leu Thr
210 215 220

His Leu Pro Gln Phe His Met Glu Ala Cys Lys Arg Leu Gln Leu Leu
225 230 235 240

Asn Ile Ser Asn Asn Tyr Val Glu Glu Leu Leu Asp Val Ala Lys Leu
245 250 255

Asp Ala Leu Tyr Asn Leu Asp Leu Ser Asp Asn Cys Leu Leu Glu His
260 265 270

Ser Gln Leu Leu Pro Leu Ser Ala Leu Met Ser Leu Ile Val Leu Asn
275 280 285

Leu Gln Gly Asn Pro Leu Ala Cys Asn Pro Lys His Arg Gln Ala Thr
290 295 300

Ala Gln Tyr Leu His Lys Asn Ser Ala Thr Val Lys Phe Val Leu Asp
305 310 315 320

Phe Glu Pro Leu Thr Lys Ala Glu Lys Ala Leu Thr Gly Ser Gln Lys
325 330 335

Trp Arg Tyr Ile Ser Gly Leu Ser His Arg Ser Pro Arg Ser Thr Ser
340 345 350

Met Ser Ile Asn Ser Ser Ser Ala Ser Ile Asn Thr Ser Asp Gly Ser
355 360 365

Gln Phe Ser Ser Phe Gly Ser Gln Arg Ser Val Ser Ile Arg Gly Lys
370 375 380

Asn Tyr Thr Leu Glu Asp Asn Gln Ser Met Asp Thr Ser Gln Ser Ser
385 390 395 400

Lys Arg Ile Ser Ser Cys Lys Ile Arg Thr Val Asp Ile Glu Glu Ser
405 410 415

Ser Glu Ile Asn Thr Asp Ala Ala Ser Val Ser Thr Pro Asn Pro Arg
420 425 430

Ser Glu Tyr Glu Glu Glu Pro Asp Asn Ser His Leu Glu Thr Lys Lys
435 440 445

Lys Ile Glu Thr Leu Arg Leu Thr Tyr Gly Asn Glu Trp Leu Lys Ser
450 455 460

Gly Asn Ala Glu Leu Met Leu Gly Ile Glu Thr Pro Gln Pro Thr Glu
465 470 475 480

Arg Glu Arg Asn Glu Ser Arg Gln Leu Phe Asn Glu Tyr Leu Gly Glu
485 490 495

Leu Ser Gly Phe Thr Glu Ala Lys Asn Asp Ser Glu His His Asn Ile
500 505 510

Ser Ser Thr Pro Thr Asn Asn Val Leu Leu Ala Ser Thr Phe Asp Ala
515 520 525

Thr Ile Thr Pro Ile Lys Ser Glu Ala Asn Asp Thr Ser Gly Gln Thr
530 535 540

Leu Tyr Glu Thr Cys Thr Glu Gly Glu Glu Thr Asn Tyr Glu Ser Phe
545 550 555 560

Gly Asn Asn Thr Thr Glu Leu Ser Thr Glu Glu Arg Pro Pro Asp Arg
565 570 575

His Glu Glu Leu Leu Arg Leu Tyr Ala Ser Ser Ser Asn Ala Gln Asp
580 585 590

Glu Asp Pro Val Ser Asp Ala Glu Ser Asp Glu Glu Thr Tyr Ile Val
595 600 605

Tyr His Glu Gln Lys Pro Ser Glu Val Leu Phe Leu Thr Ile Ser Ser
610 615 620

Asn Phe Ile Arg Glu Lys Asp Thr Leu Thr Glu Arg Thr Lys Ala Lys
625 630 635 640

Trp Ser Leu Lys Ile Leu Glu Ser Cys Glu Arg Val Arg Ser Asn Thr
645 650 655

Leu Arg Ile Asn Phe Asp Thr Met Arg Lys Asp Lys Gln Glu Arg Ile
660 665 670

Tyr Cys Val Glu Asn Thr Leu Cys Gln Glu Leu Glu Lys Lys Leu Arg
675 680 685

Asp Ile Leu Ser Gln Arg Asp Leu Thr Glu Met Asn Ile Ser Ile Tyr
690 695 700

Arg Cys Val Asn Cys Leu Thr Gln Phe Thr Ile Glu Gln Lys Ser Lys
705 710 715 720

Arg Tyr Lys Ala Lys Glu Leu Arg Cys Pro Asp Cys Arg Ser Val Tyr
725 730 735

Val Ala Glu Val Thr Glu Leu Ser Ser Ser Leu Ser Lys Pro Ser Gly
740 745 750

Glu Val Ala Ala Glu Pro Lys Leu Ser Pro Ala Met Ile Val Glu Glu
755 760 765

Ser Pro Val Glu Glu Leu Ala Ala Ala Ile Asn Lys Glu Glu Ser Asn
770 775 780

Ser Ile Gly Lys Ser Leu Ala Ser Phe Leu Phe Tyr Phe Asp Glu Ser
 785 790 795 800
 Ser Phe Asp Ser Asn Gln Ser Val Val Gly Ser Ser Asn Thr Asp Arg
 805 810 815
 Asp Met Glu Phe Arg Ala Asn Glu Ser Asp Val Asp Ile Ile Ser Asn
 820 825 830
 Pro Ser Gln Ser Ser Ile Glu Val Leu Asp Pro Asn Tyr Val Gln Ser
 835 840 845
 Ala Ser Arg Lys Thr Ser Glu Glu Arg Arg Ile Ser Gln Leu Pro His
 850 855 860
 Leu Glu Thr Ile His Asp Glu Val Ala Lys Ser Lys Ser Phe Ile Glu
 865 870 875 880
 Arg Glu Phe Gly Gln Leu Leu Ala Glu Gln Ala Gln Pro Thr Thr Pro
 885 890 895
 Ser Thr Ala Ala Pro Leu Ala Pro Ala Lys Ser Ala Val Pro Ser His
 900 905 910
 Val Pro Leu Thr Glu Ser Ser Ser Ser Gly Ser Val Thr Asp Ser Ile
 915 920 925
 Cys Thr Thr Tyr Glu Gln Gln Ala Thr Asp Ala Pro Gln Asn Leu Gln
 930 935 940
 Asn Ser Leu Leu Thr Glu Ser Ser Asn Ser Gln Val Ser Gly Ser Asp
 945 950 955 960
 Ala Glu Ser Asn Ser Arg Leu Lys Ser Ala Glu Asp Ala Ser Leu Leu
 965 970 975
 Pro Phe Ala Ser Val Phe Gln Ser Thr Asn Leu Leu Met Ser Ser Ser
 980 985 990
 Lys Lys Leu Ile Glu Ser Glu Ala Thr Val Phe Gly Thr Gln Pro Tyr
 995 1000 1005
 Lys Phe Asn Tyr Ser Asp Phe Asn Asp Ile Asp His Arg Leu Lys Leu
 1010 1015 1020
 Tyr Phe Tyr Gln Arg Lys Phe Lys Glu Asp Gly Glu His Phe Lys Trp
 1025 1030 1035 1040
 Leu Ala Lys Gly Arg Ile Tyr Asn Glu Gln Thr Gln Ser Leu Gly Glu
 1045 1050 1055
 Gly Leu Val Val Met Ser Asn Cys Lys Cys Tyr Leu Met Glu Ala Phe
 1060 1065 1070
 Ala Glu Pro His Asp Asp Val Ala Lys Trp Leu Arg Gln Val Val Ser
 1075 1080 1085

Val Ala Val Asn Arg Leu Val Ala Ile Asp Leu Leu Pro Trp Lys Leu
1090 1095 1100

Gly Leu Ser Phe Thr Leu Lys Asp Trp Gly Gly Phe Val Leu Leu Leu
1105 1110 1115 1120

His Asp Met Leu Arg Thr Glu Ser Leu Leu Asn Tyr Leu Gln Gln Ile
1125 1130 1135

Pro Leu Pro Glu Gln Cys Lys Leu Asn His Gln Pro Ser Val Thr Leu
1140 1145 1150

Ser His Gln Trp Glu Thr Ile Ala Ser Glu Pro Val Lys Met Cys Ser
1155 1160 1165

Leu Ile Pro Ser Cys Gln Trp Ile Cys Asp Gln Glu Lys Ser Ser Phe
1170 1175 1180

Glu Pro Ser Leu Leu Leu Ile Thr Glu Thr His Leu Tyr Ile Ser Gly
1185 1190 1195 1200

Asn Gly Lys Phe Ser Trp Leu Ser Asp Lys Val Gln Glu Lys Pro Ile
1205 1210 1215

Gln Pro Glu Leu Ser Leu Asn Gln Pro Leu Ser Asn Leu Val Asp Val
1220 1225 1230

Glu Arg Ile Thr Asp Gln Lys Tyr Ala Ile Asn Phe Ile Asp Glu Thr
1235 1240 1245

Gln Asn Arg Cys Glu Ile Trp Lys Leu Gln Phe Glu Thr His Ala Asn
1250 1255 1260

Ala Ala Cys Cys Leu Asn Val Ile Gly Lys Gly Trp Glu Gln Leu Phe
1265 1270 1275 1280

Gly Val Pro Phe Ser Leu Ser Gly Thr
1285